

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bander, Neil H.
- (ii) TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF
CANCER
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 - (B) STREET: Clinton Square, P.O. Box 1051
 - (C) CITY: Rochester
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 14603-1051
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/016,976
 - (B) FILING DATE: 06-MAY-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 06/022,125
 - (B) FILING DATE: 18-JUL-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/838,632
 - (B) FILING DATE: 09-APR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Goldman, Michael L.
 - (B) REGISTRATION NUMBER: 30,727
 - (C) REFERENCE/DOCKET NUMBER: 19603/1173
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:

0959545-031301
FILED

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTCCTGTCA GGAAGTGCAG GTGTCCTCTC TGAGGTCCAG CTGCAACAGT CTGGACCTGA	60
ACTGGTGAAG CCTGGGACTT CAGTGAGGAT ATCCTGCAAG ACTTCTGGAT ACACATTCAC	120
TGAATATACC ATACACTGGG TGAAGCAGAG CCATGGAAAG AGCCTTGAGT GGATTGGAAA	180
CATCAATCCT AACAAATGGTG GTACCACCTA CAATCAGAAG TTCGAGGACA AGGCCACATT	240
GACTGTAGAC AAGTCCTCCA GTACAGCCTA CATGGAGCTC CGCAGCCTAA CATCTGAGGA	300
TTCTGCAGTC TATTATTGTG CAGCTGGTTG GAACTTTGAC TACTGGGGCC AAGGCACCAC	360
TCTCACAGTC TCCTCAGCCA AAACGACACC C	391

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGTGTCGTT TTGGCTGAGG AGACTGTGAG AGTGGTGCCT TGGCCCCAGT AGTCAAAGTT	60
CCAACCAGCT GCACAATAAT AGACTGCAGA ATCCTCAGAT GTTAGGCTGC GGAGCTCCAT	120
GTAGGCTGTA CTGGAGGACT TGTCTACAGT CAATGTGGCC TTGTCCTCGA ACTTCTGATT	180
GTAGGTGGTA CCACCATTGT TAGGATTGAT GTTTCCAATC CACTCAAGGC TCTTTCCATG	240
GCTCTGCTTC ACCCAGTGTA TGGTATATTC AGTGAATGTG TATCCAGAAG TCTTGCAGGA	300
TATCCTCACT GAAGTCCCAG GCTTCACCAG TTCAGGTCCA GACTGTTGCA GCTGGACCTC	360
AGAGAGGACA CCTGCAGTTC CTAGCAGGAG A	391

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Pro Val Arg Asn Cys Arg Cys Pro Leu Gly Pro Ala Ala Thr Val
1 5 10 15
Trp Thr Thr Gly Glu Ala Trp Asp Phe Ser Glu Asp Ile Leu Gln Asp
20 25 30
Phe Trp Ile His Ile His Ile Tyr His Thr Leu Gly Glu Ala Glu Pro
35 40 45
Trp Lys Glu Pro Val Asp Trp Lys His Gln Ser Gln Trp Trp Tyr His
50 55 60
Leu Gln Ser Glu Val Arg Gly Gln Gly His Ile Asp Cys Arg Gln Val
65 70 75 80
Leu Gln Tyr Ser Leu His Gly Ala Pro Gln Pro Asn Ile Gly Phe Cys
85 90 95
Ser Leu Leu Leu Cys Ser Trp Leu Glu Leu Leu Leu Gly Pro Arg His
100 105 110
His Ser His Ser Leu Leu Ser Gln Asn Asp Thr
115 120

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Leu Ser Gly Thr Ala Gly Val Leu Ser Glu Val Gln Leu Gln Gln
1 5 10 15
Ser Gly Pro Glu Leu Val Lys Pro Gly Thr Ser Val Arg Ile Ser Cys
20 25 30
Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr Thr Ile His Trp Val Lys
35 40 45
Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Asn Ile Asn Pro Asn
50 55 60
Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe Glu Asp Lys Ala Thr Leu
65 70 75 80
Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu
85 90 95
Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Ala Gly Trp Asn Phe
100 105 110

09026545-061304

Thr Pro
130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Leu	Ser	Cys	Gln	Glu	Leu	Gln	Val	Ser	Ser	Leu	Arg	Ser	Ser	Cys	Asn
1				5				10						15	
Ser	Leu	Asp	Leu	Asn	Trp	Ser	Leu	Gly	Leu	Gln	Gly	Tyr	Pro	Ala	Arg
			20					25					30		
Leu	Leu	Asp	Thr	His	Ser	Leu	Asn	Ile	Pro	Tyr	Thr	Gly	Ser	Arg	Ala
			35				40					45			
Met	Glu	Arg	Ala	Leu	Ser	Gly	Leu	Glu	Thr	Ser	Ile	Leu	Thr	Met	Val
	50					55					60				
Val	Pro	Pro	Thr	Ile	Arg	Ser	Ser	Arg	Thr	Arg	Pro	His	Leu	Thr	Ser
65					70					75					80
Pro	Pro	Val	Gln	Pro	Thr	Trp	Ser	Ser	Ala	Ala	His	Leu	Arg	Ile	Leu
				85					90					95	
Gln	Ser	Ile	Ile	Val	Gln	Leu	Val	Gly	Thr	Leu	Thr	Thr	Gly	Ala	Lys
			100					105					110		
Ala	Pro	Leu	Ser	Gln	Pro	Ser	Gln	Pro	Lys	Arg	His	Pro			
		115					120					125			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGGTCCAGC	TGCAACAGTC	TGGACCTGAA	CTGGTGAAGC	CTGGGACTTC	AGTGAGGATA	60
TCCTGCAAGA	CTTCTGGATA	CACATTCACT	GAATATACCA	TACACTGGGT	GAAGCAGAGC	120

CATGGAAAGA GCCTTGAGTG GATTGGAAAC ATCAATCCTA ACAATGGTGG TACCACCTAC	180
AATCAGAAGT TCGAGGACAA GGCCACATTG ACTGTAGACA AGTCCTCCAG TACAGCCTAC	240
ATGGAGCTCC GCAGCCTAAC ATCTGAGGAT TCTGCAGTCT ATTATTGTGC AGCTGGTTGG	300
AACTTTGACT ACTGGGGCCA AGGCACCACT CTCACAGTCT CCTCA	345

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTGAGGAGACT GTGAGAGTGG TGCCTTGGCC CCAGTAGTCA AAGTTCCAAC CAGCTGCACA	60
ATAATAGACT GCAGAATCCT CAGATGTTAG GCTGCGGAGC TCCATGTAGG CTGTACTGGA	120
TGGACTTGTCT ACAGTCAATG TGGCCTTGTC CTCGAACCTC TGATTGTAGG TGGTACCACC	180
ATTGTTAGGA TTGATGTTTC CAATCCACTC AAGGCTCTTT CCATGGCTCT GCTTCACCCA	240
GTGTATGGTA TATTCAGTGA ATGTGTATCC AGAAGTCTTG CAGGATATCC TCACTGAAGT	300
CCCAGGCTTC ACCAGTTCAG GTCCAGACTG TTGCAGCTGG ACCTC	345

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr	15
1 5 10	
Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr	30
20 25 30	
Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile	45
35 40 45	
Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe	60
50 55 60	

Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110
Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTATATGGAG CTGATGGGAA CATTGTAATG ACCCAATCTC CCAAATCCAT GTCCATGTCA 60
GTAGGAGAGA GGGTCACCTT GACCTGCAAG GCCAGTGAGA ATGTGGTTAC TTATGTTTCC 120
TGGTATCAAC AGAAACCAGA GCAGTCTCCT AACTGCTGA TATACGGGGC ATCCAACCGG 180
TAACTGGGG TCCCGATCG CTTACAGGC AGTGGATCTG CAACAGATTT CACTCTGACC 240
ATCAGCAGTG TGCAGGCTGA AGACCTTGCA GATTATCACT GTGGACAGGG TTACAGCTAT 300
CCGTACACGT TCGGAGGGGG GACCAAGCTG GAAATAAAAC GGGCTGATGC TGCACCAACT 360
GTA 363

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACAGTTGGT GCAGCATCAG CCCGTTTTAT TTCCAGCTTG GTCCCCCTC CGAACGTGTA 60
CGGATAGCTG TAACCCTGTC CACAGTGATA ATCTGCAAGG TCTTCAGCCT GCACACTGCT 120
GATGGTCAGA GTGAAATCTG TTGCAGATCC ACTGCCTGTG AAGCGATCGG GGACCCCACT 180

GTACCGGTTG	GATGCCCCGT	ATATCAGCAG	TTTAGGAGAC	TGCTCTGGTT	TCTGTTGATA	240
CCAGGAAACA	TAAGTAACCA	CATTCTCACT	GGCCTTGCAG	GTCAAGGTGA	CCCTCTCTCC	300
TACTGACATG	GACATGGATT	TGGGAGATTG	GGTCATTACA	ATGTTCCCAT	CAGCTCCATA	360
TAA						363

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu	Tyr	Gly	Ala	Asp	Gly	Asn	Ile	Val	Met	Thr	Gln	Ser	Pro	Lys	Ser
1				5					10					15	
Met	Ser	Met	Ser	Val	Gly	Glu	Arg	Val	Thr	Leu	Thr	Cys	Lys	Ala	Ser
		20						25					30		
Glu	Asn	Val	Val	Thr	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Glu	Gln
		35					40					45			
Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val
	50					55					60				
Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Ala	Thr	Asp	Phe	Thr	Leu	Thr
65					70					75					80
Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln
				85					90					95	
Gly	Tyr	Ser	Tyr	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile
			100					105					110		
Lys	Arg	Ala	Asp	Ala	Ala	Pro	Thr	Val							
		115					120								

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Met¹ Glu Leu Met Gly Thr Leu Pro Asn Leu Pro Asn Pro Cys Pro
1 5 10 15

Cys Gln Glu Arg Gly Ser Pro Pro Ala Arg Pro Val Arg Met Trp Leu
20 25 30
Leu Met Phe Pro Gly Ile Asn Arg Asn Gln Ser Ser Leu Leu Asn Cys
35 40 45
Tyr Thr Gly His Pro Thr Gly Thr Leu Gly Ser Pro Ile Ala Ser Gln
50 55 60
Ala Val Asp Leu Gln Gln Ile Ser Leu Pro Ser Ala Val Cys Arg Leu
65 70 75 80
Lys Thr Leu Gln Ile Ile Thr Val Asp Arg Val Thr Ala Ile Arg Thr
85 90 95
Arg Ser Glu Gly Gly Pro Ser Trp Lys Asn Gly Leu Met Leu His Gln
100 105 110
Leu Tyr

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile Ile Trp Ser Trp Glu His Cys Asn Asp Pro Ile Ser Gln Ile His
1 5 10 15
Val His Val Ser Arg Arg Glu Gly His Leu Asp Leu Gln Gly Gln Glu
20 25 30
Cys Gly Tyr Leu Cys Phe Leu Val Ser Thr Glu Thr Arg Ala Val Ser
35 40 45
Thr Ala Asp Ile Arg Gly Ile Gln Pro Val His Trp Gly Pro Arg Ser
50 55 60
Leu His Arg Gln Trp Ile Cys Asn Arg Phe His Ser Asp His Gln Gln
65 70 75 80
Cys Ala Gly Arg Pro Cys Arg Leu Ser Leu Trp Thr Gly Leu Gln Leu
85 90 95
Ser Val His Val Arg Arg Gly Asp Gln Ala Gly Asn Lys Thr Gly Cys
100 105 110
Cys Thr Asn Cys
115

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AACATTGTAA TGACCCAATC TCCCAAATCC ATGTCCATGT CAGTAGGAGA GAGGGTCACC	60
TTGACCTGCA AGGCCAGTGA GAATGTGGTT ACTTATGTTT CCTGGTATCA ACAGAAACCA	120
GAGCAGTCTC CTAAACTGCT GATATACGGG GCATCCAACC GGTACACTGG GGTCCCCGAT	180
CGCTTCACAG GCAGTGGATC TGCAACAGAT TTCACTCTGA CCATCAGCAG TGTGCAGGCT	240
GAAGACCTTG CAGATTATCA CTGTGGACAG GGTTACAGCT ATCCGTACAC GTTCGGAGGG	300
GGGACCAAGC TGGAAATAAA A	321

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTTTATTTCC AGCTTGGTCC CCCCTCCGAA CGTGTACGGA TAGCTGTAAC CCTGTCCACA	60
GTGATAATCT GCAAGGTCTT CAGCCTGCAC ACTGCTGATG GTCAGAGTGA AATCTGTTGC	120
AGATCCACTG CCTGTGAAGC GATCGGGGAC CCCAGTGTAC CGGTTGGATG CCCCCTATAT	180
CAGCAGTTTA GGAGACTGCT CTGGTTTCTG TTGATACCAG GAAACATAAG TAACCACATT	240
CTCACTGGCC TTGCAGGTCA AGGTGACCCT CTCTCCTACT GACATGGACA TGGATTTGGG	300
AGATTGGGTC ATTACAATGT T	321

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
 1 5 10 15
 Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
 20 25 30
 Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile
 35 40 45
 Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60
 Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
 65 70 75 80
 Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACATTGTGA	TGACCCAGTC	TCACAAATTC	ATGTCCACAT	CAGTAGGAGA	CAGGGTCAGC	60
ATCATCTGTA	AGGCCAGTCA	AGATGTGGGT	ACTGCTGTAG	ACTGGTATCA	ACAGAAACCA	120
GGACAATCTC	CTAAACTACT	GATTTATTGG	GCATCCACTC	GGCACACTGG	AGTCCCTGAT	180
CGCTTCACAG	GCAGTGGATC	TGGGACAGAC	TTCACTCTCA	CCATTACTAA	TGTTCACTCT	240
GAAGACTTGG	CAGATTATTT	CTGTCAGCAA	TATAACAGCT	ATCCTCTCAC	GTTCCGGTGCT	300
GGGACCATGC	TGGACCTGAA	A				321

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp	Ile	Val	Met	Thr	Gln	Ser	His	Lys	Phe	Met	Ser	Thr	Ser	Val	Gly
1				5					10						15
Asp	Arg	Val	Ser	Ile	Ile	Cys	Lys	Ala	Ser	Gln	Asp	Val	Gly	Thr	Ala
			20					25					30		
Val	Asp	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile
		35				40						45			
Tyr	Trp	Ala	Ser	Thr	Arg	His	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Thr	Asn	Val	Gln	Ser
65					70					75					80
Glu	Asp	Leu	Ala	Asp	Tyr	Phe	Cys	Gln	Gln	Tyr	Asn	Ser	Tyr	Pro	Leu
				85					90					95	
Thr	Phe	Gly	Ala	Gly	Thr	Met	Leu	Asp	Leu	Lys					
			100					105							